84125

Delaval, Jan

From: Roark, Jessica
Sent: Monday, January 13, 2003 3:19 PM
To: Delaval, Jan
Subject: 09/728,911

Jan,

Please search, including pending, the following from 09/728,911:

SEQ ID NO:2
SEQ ID NO:2 as an oligo
SEQ ID NO:34
SEQ ID NO:35 and
SEQ ID NO:36.

Results on paper please.

Thanks!

Jessica H. Roark
CM1 8A03
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:34:21 ; Search time 35 Seconds
(without alignments)
879.454 Million cell updates/sec

Title: US-09-728-911-2
Perfect score: 231
Sequence: 1 MMPKHCFLGFLISFFLTGVA.....YQPMLDRRSQRSEERCVEIP 231

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	231	100.0	231	22	AAE05048	Human ZCYTO18 solu
2	231	100.0	231	22	AAE02460	Human DNAX cytokin
3	231	100.0	231	22	AAB62657	Human cytokine rec
4	231	100.0	231	23	AAO17381	Human cytokine rec
5	231	100.0	231	23	AAU80000	Human IL-TIF/IL-22
6	231	100.0	231	23	ABG34086	Human Pro peptide
7	231	100.0	231	23	AAE17320	Human cytokine rec
8	212	91.8	214	23	AAE17319	Human cytokine rec
9	210	90.9	210	22	AAB62663	Human zcytor16 ext
10	165	71.4	262	22	AAU09186	Human PRO19598 pol
11	165	71.4	263	23	AAU80324	Human IL-TIF/IL-22
12	165	71.4	263	23	AAE17321	Human cytokine rec
13	154	66.7	263	23	AAO17382	Human cytokine rec
14	105	45.5	249	22	AAE02458	Human DNAX cytokin
15	105	45.5	249	23	AAO17380	Human cytokine rec
16	97	42.0	130	22	AAE02461	Human DNAX cytokin
17	56	24.2	56	22	ABB36621	Peptide #4127 enco
18	56	24.2	56	22	ABB40797	Peptide #8303 enco
19	56	24.2	56	22	ABB24991	Protein #6990 enco
20	56	24.2	56	22	AAM61657	Human brain expres
21	56	24.2	56	22	AAM74449	Human bone marrow
22	56	24.2	56	22	AAM20320	Peptide #6754 enco
23	56	24.2	56	22	AAM34563	Peptide #8600 enco
24	56	24.2	56	23	ABG39407	Human peptide enco
25	56	24.2	56	23	ABG44337	Human peptide enco
26	7	3.0	53	22	AAG77117	Human colon cancer
27	7	3.0	87	22	AAU53889	Propionibacterium
28	7	3.0	103	22	AAU48254	Propionibacterium
29	7	3.0	151	22	AAU39711	Propionibacterium
30	7	3.0	180	23	ABB54538	Lactococcus lactis
31	7	3.0	213	23	ABB55111	Lactococcus lactis
32	7	3.0	216	23	ABB08654	Human p62cd6 prote
33	7	3.0	218	21	AAG54892	Arabidopsis thalia
34	7	3.0	223	21	AAG44613	Zea mays protein f
35	7	3.0	227	21	AAG44612	Zea mays protein f
36	7	3.0	233	21	AAG40916	Zea mays protein f
37	7	3.0	237	21	AAG40915	Zea mays protein f
38	7	3.0	270	22	AAG71862	Human olfactory re
39	7	3.0	270	22	AAG72529	Human OR-like poly
40	7	3.0	287	22	AAG74001	Human colon cancer
41	7	3.0	319	22	AAE11912	Human G-protein co
42	7	3.0	323	23	ABB92486	Herbicidally activ
43	7	3.0	341	19	AAW98546	H. pylori GHPO 156
44	7	3.0	426	21	AAG53516	Arabidopsis thalia
45	7	3.0	470	22	ABB68836	Drosophila melanog
46	7	3.0	490	21	AAG53515	Arabidopsis thalia
47	7	3.0	495	22	ABB65066	Drosophila melanog
48	7	3.0	518	21	AAG53514	Arabidopsis thalia
49	7	3.0	589	22	ABG10847	Novel human diagno
50	7	3.0	875	22	ABG08151	Novel human diagno
51	7	3.0	1192	22	AAU35310	Enterococcus faeca
52	6	2.6	14	22	AAM97253	Human peptide #528
53	6	2.6	14	22	AAM97626	Human peptide #901
54	6	2.6	15	20	AAY30497	Mutant sequence of
55	6	2.6	15	20	AAY30511	Mutant sequence of
56	6	2.6	15	20	AAY30512	Mutant sequence of
57	6	2.6	25	23	ABG62277	Eubacterial DNA po
58	6	2.6	29	21	AAB28281	Human secreted pep
59	6	2.6	30	13	AAR25225	Residues 174-203 o
60	6	2.6	35	20	AAW92292	Human alpha-1 (XVI
61	6	2.6	36	22	AAM88692	Human immune/haema
62	6	2.6	37	22	AAB99012	Barley PSI-N trans
63	6	2.6	39	20	AAW82461	Murine Cu/Zn SOD e
64	6	2.6	39	21	AAB52049	Human secreted pro
65	6	2.6	42	20	AAY12368	Human 5' EST secre
66	6	2.6	42	23	ABP27534	Streptococcus poly
67	6	2.6	43	20	AAY36312	Human secreted pro
68	6	2.6	43	22	AAM94625	Human reproductive
69	6	2.6	43	22	AAM42257	Human breast or ov
70	6	2.6	45	19	AAW79315	Staphylococcus aur
71	6	2.6	48	21	AAG15174	Arabidopsis thalia
72	6	2.6	48	22	AAU14766	Novel bone marrow
73	6	2.6	52	18	AAW19035	F-T1-SP10MN(A) reg
74	6	2.6	52	22	AAU43049	Propionibacterium
75	6	2.6	52	22	AAU55234	Propionibacterium
76	6	2.6	53	18	AAW19038	F-T1-SP10IIIB(A) r
77	6	2.6	53	23	ABP31389	Human ORF362 prote
78	6	2.6	54	21	AAG16413	Arabidopsis thalia
79	6	2.6	55	22	AAU56892	Propionibacterium
80	6	2.6	55	22	AAU65128	Propionibacterium
81	6	2.6	56	19	AAY85999	S. pneumoniae deri
82	6	2.6	57	21	AAG00498	Human secreted pro
83	6	2.6	57	23	ABP33289	Human ORF2262 prot

84	6	2.6	58	22	AAM89102	Human immune/haema
85	6	2.6	59	21	AAY76330	Fragment of human
86	6	2.6	59	22	AAO09410	Human polypeptide
87	6	2.6	61	23	ABP03236	Human ORFX protein
88	6	2.6	64	22	AAU52005	Propionibacterium
89	6	2.6	64	22	AAG74813	Human colon cancer
90	6	2.6	65	22	ABB96568	Human testicular a
91	6	2.6	65	22	AAM96564	Human reproductive
92	6	2.6	66	21	AAG41178	Zea mays protein f
93	6	2.6	66	22	AAU46335	Propionibacterium
94	6	2.6	67	22	AAO13356	Human polypeptide
95	6	2.6	68	22	AAU20237	Human novel endocr
96	6	2.6	70	22	AAM92880	Human digestive sy
97	6	2.6	73	22	ABG18265	Novel human diagno
98	6	2.6	76	19	AAY20295	Human apolipoprote
99	6	2.6	76	22	AAM82738	Human immune/haema
100	6	2.6	77	22	ABG26679	Novel human diagno

ALIGNMENTS

RESULT 1
AAE05048
ID AAE05048 standard; Protein; 231 AA.
XX
AC AAE05048;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human ZCYTO18 soluble receptor antagonist, zcytor16 protein.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; zcytor16.
XX
OS Homo sapiens.
XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35308.
XX
PR 23-DEC-1999; 99US-0471767.
PR 01-DEC-2000; 2000US-0250841.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
DR N-PSDB; AAD09745.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS Example 13A; Page 158-159; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC killing cancer cells. It is useful for increasing platelets in a
CC patient or injured tissue. It is also used in gene therapy.
CC The present sequence is human zcytor16, which is a naturally expressed
CC soluble receptor antagonist of ZCYTO18 protein.
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 231; DB 22; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e-220;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
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Db      1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
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Db     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
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Db    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180

Qy    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 2
AAE02460
ID AAE02460 standard; Protein; 231 AA.
XX
AC AAE02460;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human DNAX cytokine receptor subunit 4.2 (DCRS4.2).
XX
KW Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
KW therapy; immunological disorder; drug screening; cell development;
KW chromosome 6q24.1-25.2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Signal-peptide
FT Protein 22..231
FT /label= DCRS4.2
FT /note= "Human mature DNAX cytokine receptor
FT subunit 4.2"
XX
PN WO200136467-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US31363.
XX
PR 18-NOV-1999; 99US-0443060.
PR 13-DEC-1999; 99US-0170320.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2001-343800/36.
DR N-PSDB; AAD06414.
XX
PT New mammalian receptor proteins related to cytokine receptors, useful
PT for regulating cell development and for diagnosis and treatment of
PT immunological disorders -
XX
PS Claim 3; Page 23; 124pp; English.
XX
CC The present sequence is human DNAX cytokine receptor subunit 4.2
CC (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2.
CC Cytokine receptors, fragments and antibodies are useful for treating
CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC useful in drug screening to identify compounds having binding affinity
CC to the receptor subunit. Modulators of DCRS are useful for modulating
CC the physiology or development of a cell or tissue culture cells. A
CC purified DCRS is useful as a reagent to detect antibodies generated in
CC response to the presence of elevated levels of expression, or

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CC   immunological disorders which lead to production of antibody to the
CC   endogenous receptor. Cytokine receptor sequences are useful as probes
CC   for detecting levels of the cytokine receptor in patients suspected of
CC   having an immunological disorder. Antibodies have therapeutic value, are
CC   useful as potent antagonist, in detecting or quantifying ligands, for
CC   isolating DCRS proteins and peptides, to screen expression libraries for
CC   particular expression products, to raise anti-idiotypic antibodies and
CC   for detecting or diagnosing various immunological conditions related to
CC   expression of the protein or cells which express the protein.
XX
SQ   Sequence   231 AA;

  Query Match             100.0%;  Score 231;  DB 22;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-220;
  Matches  231;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
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Qy    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
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Qy    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231


RESULT 3
AAB62657
ID   AAB62657 standard; Protein; 231 AA.
XX
AC   AAB62657;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Human cytokine receptor, zcytor16.
XX
KW   Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW   antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW   immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          22..108
FT                   /note= "Ig domain 1"
FT   Domain          22..231
FT                   /note= "extracellular domain"
FT   Domain          112..210
FT                   /note= "Ig domain 2"
XX
PN   WO200140467-A1.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32703.
XX
PR   03-DEC-1999;   99US-0169049.
PR   13-SEP-2000; 2000US-0232219.
PR   31-OCT-2000; 2000US-0244610.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Xu W,  Kindsvogel W,  Chen Z;
XX
DR   WPI; 2001-356158/37.
DR   N-PSDB; AAF83735.
XX
PT   New soluble cytokine receptor polypeptides and polynucleotides, useful
PT   for diagnosing and treating cancer and inflammatory conditions -
XX
PS   Claim 1; Page 186-188; 210pp; English.
XX
CC   The invention relates to a human cytokine receptor polypeptide,
CC   designated zcytor16. The zcytor16 polypeptide can be expressed by
CC   standard recombinant methodology and can bind to IL-TIF (undefined). The
CC   zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC   or differentiation of hematopoietic cell(s) (progenitors); reducing
CC   IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC   inflammatory response in a mammal with inflammation. Heteromeric/
CC   multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC   used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC   can also be used to detect IL-TIF levels which is indicative of
CC   pathological conditions including inflammatory states (e.g. rheumatoid
CC   arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC   polypeptides themselves are useful for the treatment of inflammation,
CC   inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC   disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC   diseases. The antibodies and zcytor16 polynucleotides are also useful
CC   for detecting cancer. The present sequence represents the human
CC   zcytor16 protein.
XX
SQ   Sequence   231 AA;

  Query Match             100.0%;  Score 231;  DB 22;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-220;
  Matches  231;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180

Qy    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231


RESULT 4
AAO17381
ID   AAO17381 standard; Protein; 231 AA.
XX
AC   AAO17381;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human cytokine receptor variant 2.
XX
KW   Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW   rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW   ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW   immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiulcer; cytostatic; dermatological;
KW   chromosome 6q24.1-25.2; receptor.
XX
OS   Homo sapiens.
XX
PN   EP1191035-A2.
XX
PD   27-MAR-2002.
XX
PF   24-AUG-2001; 2001EP-0250307.
XX
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PR 25-SEP-2000; 2000DE-1048626.
PR 17-NOV-2000; 2000DE-1058907.
PR 19-DEC-2000; 2000DE-1064906.
XX
PA (SCHD) SCHERING AG.
XX
PI Weiss B, Sabat R, Assadullah K, Toshi L;
XX
DR WPI; 2002-332210/37.
DR N-PSDB; AAL46000.
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
PS Claim 6; Page 14; 21pp; German.
XX
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the
CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC variant 2 of the invention.
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 231; DB 23; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e-220;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
Db 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy 61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
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Qy 121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
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Qy 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
Db 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231

RESULT 5
AAU80000
ID AAU80000 standard; Protein; 231 AA.
XX
AC AAU80000;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human IL-TIF/IL-22 binding protein #1.
XX
KW Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
KW IL-TIF/IL-22 antagonist.
XX
OS Homo sapiens.
XX
PN WO200224912-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US29576.
XX
PR 22-SEP-2000; 2000US-234583P.
PR 03-NOV-2000; 2000US-245495P.
PR 31-JUL-2001; 2001US-0919162.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Renauld J, Dumoutier L;
XX
DR WPI; 2002-383190/41.
DR N-PSDB; ABK50076.
XX
PT Polynucleotide and polypeptide of soluble protein which binds to
PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT cell -
XX
PS Claim 14; Page 39; 42pp; English.
XX
CC The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present amino
CC acid sequence represents the human IL-TIF/IL-22 binding protein #1 of
CC the invention.
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 231; DB 23; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e-220;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
Db 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy 61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
Db 61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy 121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
Db 121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180

Qy 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
Db 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231

RESULT 6
ABG34086
ID ABG34086 standard; Protein; 231 AA.
XX
AC ABG34086;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Pro peptide #57.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX

PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27099.
XX
PR 01-SEP-2000; 2000US-229896P.
PR 05-SEP-2000; 2000US-230621P.
PR 22-SEP-2000; 2000US-235147P.
PR 10-NOV-2000; 2000WO-US30873.
PR 12-JAN-2001; 2001US-261878P.
PR 16-JAN-2001; 2001US-261910P.
PR 16-JAN-2001; 2001US-261939P.
PR 16-JAN-2001; 2001US-262150P.
PR 25-JAN-2001; 2001US-264395P.
PR 02-FEB-2001; 2001US-266421P.
PR 09-FEB-2001; 2001US-267623P.
PR 28-FEB-2001; 2001WO-US06520.
PR 09-MAR-2001; 2001US-274399P.
PR 03-APR-2001; 2001US-280982P.
PR [redacted]4-APR-2001; 2001US-282129P.
PR [redacted]4-APR-2001; 2001US-282199P.
PR 09-MAY-2001; 2001US-290589P.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2002-362426/39.
DR N-PSDB; ABK70017.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or
PT for genetic analysis of individuals with genetic disorders -
XX
PS Claim 11; Figure 114; 218pp; English.
XX
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The
CC invention also comprises a method for producing the proteins of the
CC invention by recombinant means and antibodies specific for the protein
CC [redacted]f the invention. The antibody may be used for detecting the PRO
CC [redacted]roteins of the invention and may be used to modify their activity.
CC polynucleotides may be used as hybridisation probes for a cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to
CC construct hybridisation probes for mapping the gene which encodes that
CC PRO and for genetic analysis of individuals with genetic disorders, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knock-out animals which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides are useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. The sequences may
CC also be used to detect overexpression on PRO polypeptides in cancerous
CC tumours and for screening for differentially expressed genes using
CC microarray technology. The present sequence represents a human PRO
CC protein of the invention.
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 231; DB 23; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e-220;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy 61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy 121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180

Qy 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231

RESULT 7
AAE17320
ID AAE17320 standard; Protein; 231 AA.
XX
AC AAE17320;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor protein, sbg456548CytoRa #2.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor.
XX
OS Homo sapiens.
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR N-PSDB; AAD27815.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 1; Page 132-133; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing

CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor.
XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 231; DB 23; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e-220;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy      61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy     121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180

Qy     181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
```

RESULT 8
AAE17319
ID AAE17319 standard; Protein; 214 AA.
XX
AC AAE17319;
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor protein, sbg456548CytoRa #1.
XX
KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor.
XX
OS Homo sapiens.
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR N-PSDB; AAD27814.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 1; Page 122; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor.
XX
SQ Sequence 214 AA;

Query Match 91.8%; Score 212; DB 23; Length 214;
Best Local Similarity 100.0%; Pred. No. 5.2e-201;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      20 AGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIYGQRQWKNKEDCW 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 AGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIYGQRQWKNKEDCW 62

Qy      80 GTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVN 139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 GTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVN 122

Qy     140 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEAL 199
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 GSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEAL 182

Qy     200 TPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
           ||||||||||||||||||||||||||||||||
Db     183 TPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 214


RESULT 9
AAB62663
ID   AAB62663 standard; Protein; 210 AA.
XX
AC   AAB62663;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Human zcytor16 extracellular domain fragment (residues 22-231).
XX
KW   Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW   antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW   immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS   Homo sapiens.
XX
PN   WO200140467-A1.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32703.
XX
PR   03-DEC-1999;   99US-0169049.
PR   13-SEP-2000; 2000US-0232219.
PR   31-OCT-2000; 2000US-0244610.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Xu W,  Kindsvogel W,  Chen Z;
XX
DR   WPI; 2001-356158/37.
XX
PT   New soluble cytokine receptor polypeptides and polynucleotides, useful
PT   for diagnosing and treating cancer and inflammatory conditions -
XX
PS   Claim 1; Page 193; 210pp; English.
XX
CC   The invention relates to a human cytokine receptor polypeptide,
CC   designated zcytor16. The zcytor16 polypeptide can be expressed by
CC   standard recombinant methodology and can bind to IL-TIF (undefined). The
CC   zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC   or differentiation of hematopoietic cell(s) (progenitors); reducing
CC   IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC   inflammatory response in a mammal with inflammation. Heteromeric/
CC   multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC   used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC   can also be used to detect IL-TIF levels which is indicative of
CC   pathological conditions including inflammatory states (e.g. rheumatoid
CC   arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC   polypeptides themselves are useful for the treatment of inflammation,
CC   inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC   disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC   diseases. The antibodies and zcytor16 polynucleotides are also useful
CC   for detecting cancer. The present sequence represents the human zcytor16
CC   extracellular domain fragment.
XX
SQ   Sequence   210 AA;

  Query Match             90.9%;  Score 210;  DB 22;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-199;
  Matches  210;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      22 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIYGQRQWKNKEDCWGT 81
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIYGQRQWKNKEDCWGT 60

Qy      82 QELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGS 141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGS 120

Qy     142 LLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTP 201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTP 180

Qy     202 HSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
           ||||||||||||||||||||||||||||||
Db     181 HSSYCVVAEIYQPMLDRRSQRSEERCVEIP 210


RESULT 10
AAU09186
ID   AAU09186 standard; Protein; 262 AA.
XX
AC   AAU09186;
XX
DT   16-JAN-2002  (first entry)
XX
DE   Human PRO19598 polypeptide.
XX
KW   Human; PRO19598; clone DNA145887; immune-related disorder;
KW   inflammatory disorder; infectious disorder; immunodeficiency disorder;
KW   autoimmune disorder; renal disease; demyelinating disease; skin disease;
KW   neoplasia; transplantation associated disease; immunosuppressive;
KW   anti-inflammatory; antiasthmatic; antidiabetic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Signal_peptide
FT   Modified-site   17..22
FT                   /note= "N-myristoylation site"
FT   Modified-site   20..25
FT                   /note= "N-myristoylation site"
FT   Protein         21..262
FT                   /label= Mature_PRO19598_polypeptide
FT   Modified-site   55..58
FT                   /note= "N-glycosylation site"
FT   Modified-site   165..168
FT                   /note= "N-glycosylation site"
FT   Modified-site   170..173
FT                   /note= "N-glycosylation site"
FT   Modified-site   191..194
FT                   /note= "N-glycosylation site"
FT   Modified-site   208..211
FT                   /note= "N-glycosylation site"
FT   Modified-site   220..225
FT                   /note= "N-myristoylation site"
XX
PN   WO200166740-A2.
XX
PD   13-SEP-2001.
XX
PF   01-MAR-2001; 2001WO-US06666.
XX
PR   03-MAR-2000; 2000US-187202P.
PR   21-MAR-2000; 2000US-191015P.
PR   30-MAY-2000; 2000WO-US14941.
PR   05-JUN-2000; 2000US-209832P.
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Fong S,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL;
PI   Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-625876/72.
```

```
DR   N-PSDB; AAS15368.
XX
PT   Nucleic acids encoding PRO polypeptides, useful for detecting and
PT   treating immune related diseases and disorders in mammals including
PT   autoimmune diseases, inflammatory diseases and asthma -
XX
PS   Claim 10; Fig 18; 122pp; English.
XX
CC   The present invention relates to the isolation of 9 novel human PRO
CC   polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.
CC   The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
CC   PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
CC   encoding these PRO polypeptides have been designated as clones
CC   DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273,
CC   DNA92223-2567, DNA96973, DNA101921 and DNA145887 respectively.
CC   Compositions (e.g. vaccines) containing PRO polypeptides and methods of
CC   using these compositions are useful in the treatment and diagnosis of
CC   immune-related disorders. Such disorders include immune-mediated
CC   inflammatory disorders (e.g. osteoarthritis), non-immune-mediated
CC   inflammatory  disorders (e.g. diabetes mellitus), infectious disorders
CC   (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS),
CC   autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal
CC   diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or
CC   central nervous system (e.g. Guillain-Barre syndrome), immune-mediated
CC   skin diseases (e.g. contact dermatitis), neoplasias and transplantation
CC   associated diseases. The polynucleotide sequences of the invention may
CC   be used in gene therapy. AAU09178-AAU09186 represent the novel human
CC   PRO polypeptides of the invention.
XX
SQ   Sequence   262 AA;

  Query Match             71.4%;  Score 165;  DB 22;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-154;
  Matches  165;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 157

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 217

Qy     187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
           |||||||||||||||||||||||||||||||||||||||||||||
Db     218 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 262


RESULT 11
AAU80324
ID   AAU80324 standard; Protein; 263 AA.
XX
AC   AAU80324;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human IL-TIF/IL-22 binding protein #2.
XX
KW   Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
KW   IL-TIF/IL-22 antagonist.
XX
OS   Homo sapiens.
XX
PN   WO200224912-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-US29576.
XX
PR   22-SEP-2000; 2000US-234583P.
PR   03-NOV-2000; 2000US-245495P.
PR   31-JUL-2001; 2001US-0919162.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Renauld J,  Dumoutier L;
XX
DR   WPI; 2002-383190/41.
DR   N-PSDB; ABK50080.
XX
PT   Polynucleotide and polypeptide of soluble protein which binds to
PT   interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT   cell -
XX
PS   Claim 14; Page 41-42; 42pp; English.
XX
CC   The present invention relates to a new polynucleotide that encodes a
CC   soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC   to as IL-22BP), where the complementary sequence of the invention
CC   hybridises under stringent conditions to a nucleotide sequence of 2271
CC   or 2366 base pairs, as given in the specification. The molecules of the
CC   invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC   on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC   for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC   in vitro, and for obtaining an antibody molecule specific for the soluble
CC   binding protein of the invention, from a population or panel of antibody
CC   molecules of diverse binding specificity. The soluble protein is further
CC   useful in manufacture of a medicament for treating an IL-22 mediated
CC   disease and for assaying an agent, preferably an antibody or a peptide
CC   fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC   of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC   used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC   disorder. The antibody is useful for determining presence of the soluble
CC   protein, where the antibody is detectably labelled. The present amino
CC   acid sequence represents the human IL-TIF/IL-22 binding protein #2 of
CC   the invention.
XX
SQ   Sequence   263 AA;

  Query Match             71.4%;  Score 165;  DB 23;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-154;
  Matches  165;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      67 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      99 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 158

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 218

Qy     187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
           |||||||||||||||||||||||||||||||||||||||||||||
Db     219 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 263


RESULT 12
AAE17321
ID   AAE17321 standard; Protein; 263 AA.
XX
AC   AAE17321;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human cytokine receptor protein, sbg456548CytoRa #3.
XX
KW   Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW   autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW   Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW   multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW   ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW   depression; cardiovascular disease; myocardial infarction; renal failure;
KW   respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW   type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW   hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
KW   nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
```

KW haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor.
XX
OS Homo sapiens.
XX
PN WO200198342-A1.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US19929.
XX
PR 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI [redacted]urdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX
DR WPI; 2002-139783/18.
DR N-PSDB; AAD27816.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities -
XX
PS Claim 1; Page 133-134; 138pp; English.
XX
CC The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesteryl ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROa-associated disorders,
CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft verse host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC [redacted]rain disorders including parasupranuclear palsy, myotonic dystrophy,
CC [redacted]epression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
CC The present sequence is human cytokine receptor.
XX
SQ Sequence 263 AA;

Query Match 71.4%; Score 165; DB 23; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.5e-154;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 126
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 99 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 158

Qy 127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 218

Qy 187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
|||||||||||||||||||||||||||||||||||||||||||||
Db 219 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 263

RESULT 13
AAO17382
ID AAO17382 standard; Protein; 263 AA.
XX
AC AAO17382;
XX
DT 08-AUG-2002 (first entry)
XX
DE Human cytokine receptor variant 3.
XX
KW Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiulcer; cytostatic; dermatological;
KW chromosome 6q24.1-25.2; receptor.
XX
OS Homo sapiens.
XX
PN EP1191035-A2.
XX
PD 27-MAR-2002.
XX
PF 24-AUG-2001; 2001EP-0250307.
XX
PR 25-SEP-2000; 2000DE-1048626.
PR 17-NOV-2000; 2000DE-1058907.
PR 19-DEC-2000; 2000DE-1064906.
XX
PA (SCHD) SCHERING AG.
XX
PI Weiss B, Sabat R, Assadullah K, Toshi L;
XX
DR WPI; 2002-332210/37.
DR N-PSDB; AAL46001.
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
PS Claim 6; Page 15; 21pp; German.
XX
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the
CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC variant 3 of the invention.
XX
SQ Sequence 263 AA;

Query Match 66.7%; Score 154; DB 23; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 126
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 99 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 158

Qy 127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 218

```
Qy    187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRS 220
          ||||||||||||||||||||||||||||||||||||
Db    219 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRS 252


RESULT 14
AAE02458
ID   AAE02458 standard; Protein; 249 AA.
XX
AC   AAE02458;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human DNAX cytokine receptor subunit 4.1 (DCRS4.1).
XX
KW   Human; immunomodulator; DNAX cytokine receptor subunit 4.1; DCRS4.1;
KW   therapy; immunological disorder; drug screening; cell development;
KW   chromosome 6q24.1-25.2.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /label= Signal-peptide
FT   Protein         22..249
FT                   /label= DCRS4.1
FT                   /note= "Human mature DNAX cytokine receptor
FT                   subunit 4.1"
FT   Modified-site   24
FT                   /note= "CK2 phosphorylation site"
FT   Modified-site   25
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   28
FT                   /note= "PKC phosphorylation site"
FT   Domain          31..70
FT                   /label= Cytokine_receptor_domain
FT   Modified-site   51
FT                   /note= "cAMP PK site"
FT   Modified-site   56
FT                   /note= "N-glycosylated"
FT   Disulfide-bond  78..86
FT                   /label= Conserved_disulphide_linkage
FT   Modified-site   81
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   85
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   89
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   92
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   100
FT                   /note= "Amidation site"
FT   Modified-site   110
FT                   /note= "Myristoyl site"
FT   Modified-site   118
FT                   /note= "PKC phosphorylation site"
FT   Modified-site   119
FT                   /note= "cAMP phosphorylation site"
FT   Modified-site   119
FT                   /note= "cAMP PK site"
FT   Modified-site   124
FT                   /note= "Myristoyl site"
FT   Modified-site   127
FT                   /note= "cAMP PK site"
FT   Modified-site   152
FT                   /note= "N-glycosylated"
FT   Modified-site   157
FT                   /note= "N-glycosylated"
FT   Modified-site   177
FT                   /note= "cAMP PK site"
FT   Modified-site   178
FT                   /note= "N-glycosylated"
FT   Modified-site   180
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   180
FT                   /note= "CK2 phosphorylation site"
FT   Modified-site   195
FT                   /note= "N-glycosylated"
FT   Modified-site   197
FT                   /note= "Calcium phosphorylation site"
FT   Modified-site   207
FT                   /note= "Myristoyl site"
FT   Modified-site   238
FT                   /note= "PKC phosphorylation site"
FT   Modified-site   241
FT                   /note= "Calcium phosphorylation site"
XX
PN   WO200136467-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31363.
XX
PR   18-NOV-1999;   99US-0443060.
PR   13-DEC-1999;   99US-0170320.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM;
XX
DR   WPI; 2001-343800/36.
DR   N-PSDB; AAD06410.
XX
PT   New mammalian receptor proteins related to cytokine receptors, useful
PT   for regulating cell development and for diagnosis and treatment of
PT   immunological disorders  -
XX
PS   Claim 3; Page 22; 124pp; English.
XX
CC   The present sequence is human DNAX cytokine receptor subunit 4.1
CC   (DCRS4.1). DCRS4 gene is located on chromosome 6q24.1-25.2.
CC   Cytokine receptors, fragments and antibodies are useful for treating
CC   immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC   useful in drug screening to identify compounds having binding affinity
CC   to the receptor subunit. Modulators of DCRS are useful for modulating
CC   the physiology or development of a cell or tissue culture cells. A
CC   purified DCRS is useful as a reagent to detect antibodies generated in
CC   response to the presence of elevated levels of expression, or
CC   immunological disorders which lead to production of antibody to the
CC   endogenous receptor. Cytokine receptor sequences are useful as probes
CC   for detecting levels of the cytokine receptor in patients suspected of
CC   having an immunological disorder. Antibodies have therapeutic value, are
CC   useful as potent antagonist, in detecting or quantifying ligands, for
CC   isolating DCRS proteins and peptides, to screen expression libraries for
CC   particular expression products, to raise anti-idiotypic antibodies and
CC   for detecting or diagnosing various immunological conditions related to
CC   expression of the protein or cells which express the protein.
XX
SQ   Sequence   249 AA;

  Query Match             45.5%;  Score 105;  DB 22;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-95;
  Matches  105;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 204

Qy    187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||
Db    205 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 249


RESULT 15
AAO17380
```

```
ID   AAO17380 standard; Protein; 249 AA.
XX
AC   AAO17380;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human cytokine receptor variant 1.
XX
KW   Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW   rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW   ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW   immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiulcer; cytostatic; dermatological;
KW   chromosome 6q24.1-25.2; receptor.
XX
OS   Homo sapiens.
XX
PN   EP1191035-A2.
XX
PD   27-MAR-2002.
XX
PF   24-AUG-2001; 2001EP-0250307.
XX
PR   25-SEP-2000; 2000DE-1048626.
PR   17-NOV-2000; 2000DE-1058907.
PR   19-DEC-2000; 2000DE-1064906.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Sabat R,  Assadullah K,  Toshi L;
XX
DR   WPI; 2002-332210/37.
DR   N-PSDB; AAL45999.
XX
PT   New nucleic acid encoding soluble cytokine receptor, useful for
PT   diagnosis and treatment of e.g. immune disease, also related protein
PT   and antibodies  -
XX
PS   Claim 6; Page 12-13; 21pp; German.
XX
CC   The present invention provides the protein and coding sequences of 3
CC   variants of a human cytokine receptor. The sequences can be used in the
CC   diagnosis, prevention and treatment of immune diseases, including
CC   psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC   arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC   transplant rejection and in reproductive medicine, e.g. for diagnosing
CC   abnormal immune reactions which cause abortions. The present sequence is
CC   variant 1 of the invention.
XX
SQ   Sequence   249 AA;

  Query Match             45.5%;  Score 105;  DB 23;  Length 249;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-95;
  Matches  105;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 204

Qy     187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||
Db     205 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 249


RESULT 16
AAE02461
ID   AAE02461 standard; Protein; 130 AA.
XX
AC   AAE02461;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human DNAX cytokine receptor subunit 4.3 (DCRS4.3).
XX
KW   Human; immunomodulator; DNAX cytokine receptor subunit 4.3; DCRS4.3;
KW   therapy; immunological disorder; drug screening; cell development;
KW   chromosome 6q24.1-25.2.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /label= Signal-peptide
FT   Protein         22..130
FT                   /label= DCRS4.3
FT                   /note= "Human mature DNAX cytokine receptor
FT                   subunit 4.3"
XX
PN   WO200136467-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31363.
XX
PR   18-NOV-1999;   99US-0443060.
PR   13-DEC-1999;   99US-0170320.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM;
XX
DR   WPI; 2001-343800/36.
DR   N-PSDB; AAD06416.
XX
PT   New mammalian receptor proteins related to cytokine receptors, useful
PT   for regulating cell development and for diagnosis and treatment of
PT   immunological disorders  -
XX
PS   Claim 3; Page 24; 124pp; English.
XX
CC   The present sequence is human DNAX cytokine receptor subunit 4.3
CC   (DCRS4.3). DCRS4 gene is located on chromosome 6q24.1-25.2.
CC   Cytokine receptors, fragments and antibodies are useful for treating
CC   immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
CC   useful in drug screening to identify compounds having binding affinity
CC   to the receptor subunit. Modulators of DCRS are useful for modulating
CC   the physiology or development of a cell or tissue culture cells. A
CC   purified DCRS is useful as a reagent to detect antibodies generated in
CC   response to the presence of elevated levels of expression, or
CC   immunological disorders which lead to production of antibody to the
CC   endogenous receptor. Cytokine receptor sequences are useful as probes
CC   for detecting levels of the cytokine receptor in patients suspected of
CC   having an immunological disorder. Antibodies have therapeutic value, are
CC   useful as potent antagonist, in detecting or quantifying ligands, for
CC   isolating DCRS proteins and peptides, to screen expression libraries for
CC   particular expression products, to raise anti-idiotypic antibodies and
CC   for detecting or diagnosing various immunological conditions related to
CC   expression of the protein or cells which express the protein.
XX
SQ   Sequence   130 AA;

  Query Match             42.0%;  Score 97;  DB 22;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-87;
  Matches   97;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy      61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQE 97
          |||||||||||||||||||||||||||||||||||||
Db      61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQE 97


RESULT 17
ABB36621
```

```
ID   ABB36621 standard; Peptide; 56 AA.
XX
AC   ABB36621;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #4127 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 27; SEQ ID NO 29256; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a peptide encoded by a single exon
CC   nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   56 AA;

  Query Match             24.2%;  Score 56;  DB 22;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-47;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56


RESULT 18
ABB40797
ID   ABB40797 standard; Peptide; 56 AA.
XX
AC   ABB40797;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #8303 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 27; SEQ ID NO 33432; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a peptide encoded by a single exon
CC   nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   56 AA;

  Query Match             24.2%;  Score 56;  DB 22;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-47;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56


RESULT 19
ABB24991
ID   ABB24991 standard; Protein; 56 AA.
XX
AC   ABB24991;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Protein #6990 encoded by probe for measuring heart cell gene expression.
XX
KW   Human; gene expression; heart; microarray; vascular system;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
```

PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 15; SEQ ID No 26761; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 56 AA;

Query Match 24.2%; Score 56; DB 22; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56

RESULT 20
AAM61657
ID AAM61657 standard; Protein; 56 AA.
XX
AC AAM61657;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33762.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 33762; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 56 AA;

Query Match 24.2%; Score 56; DB 22; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56

RESULT 21
AAM74449
ID AAM74449 standard; Protein; 56 AA.
XX
AC AAM74449;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34755.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 34755; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
XX
SQ Sequence 56 AA;

```
  Query Match             24.2%;  Score 56;  DB 22;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-47;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56


RESULT 22
AAM20320
ID   AAM20320 standard; Protein; 56 AA.
XX
AC   AAM20320;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Peptide #6754 encoded by probe for measuring cervical gene expression.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 27; SEQ ID No 25146; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC   by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC   can be used to produce a single exon microarray, which can be used for
CC   measuring human gene expression in a sample derived from human cervical
CC   epithelial cells. By measuring gene expression, the probes are therefore
CC   useful in grading and/or staging of diseases of the cervix, notably
CC   cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   56 AA;

  Query Match             24.2%;  Score 56;  DB 22;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-47;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56


RESULT 23
AAM34563
ID   AAM34563 standard; Protein; 56 AA.
XX
AC   AAM34563;
XX
DT   17-OCT-2001  (first entry)
XX
DE   Peptide #8600 encoded by probe for measuring placental gene expression.
XX
KW   Probe; microarray; human; placenta; antenatal diagnosis;
KW   genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200157272-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00663.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488897/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human placenta -
XX
PS   Claim 27; SEQ ID No 34832; 654pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes (SENP:
CC   see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for producing a microarray for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from human placenta. The probes are useful for antenatal diagnosis of
CC   human genetic disorders.
XX
SQ   Sequence   56 AA;

  Query Match             24.2%;  Score 56;  DB 22;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-47;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56


RESULT 24
ABG39407
ID   ABG39407 standard; Peptide; 56 AA.
XX
AC   ABG39407;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 29072.
XX
KW   Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW   chronic obstructive pulmonary disease; interstitial lung disease;
KW   familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW   tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW   pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
```

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA [redacted](MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 27; SEQ ID No 29072; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 56 AA;

Query Match 24.2%; Score 56; DB 23; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56

RESULT 25
ABG44337
ID ABG44337 standard; Peptide; 56 AA.
XX
AC ABG44337;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34002.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 27; SEQ ID No 34002; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 56 AA;

Query Match 24.2%; Score 56; DB 23; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 182
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEK 56

RESULT 26
AAG77117
ID AAG77117 standard; Protein; 53 AA.
XX
AC AAG77117;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:7881.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR N-PSDB; AAH36522.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 11; Page 9219-9220; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 53 AA;

Query Match 3.0%; Score 7; DB 22; Length 53;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 ALTGNSS 58
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Db 2 ALTGNSS 8

RESULT 27
AAU53889
ID AAU53889 standard; Protein; 87 AA.
XX
AC AAU53889;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #14785.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
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PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59562.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 15084; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:47:22 ; Search time 10 Seconds
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Title: US-09-728-911-2
Perfect score: 231
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 118974 seqs, 19401057 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	56	24.2	56	10	US-09-864-761-47623	Sequence 47623, A
6	7	3.0	270	10	US-09-823-356-11	Sequence 11, Appl
7	7	3.0	341	9	US-09-895-913A-322	Sequence 322, App
8	7	3.0	1192	10	US-09-815-242-10903	Sequence 10903, A
9	7	3.0	2771	9	US-09-808-602-82	Sequence 82, Appl
10	6	2.6	84	10	US-09-864-761-39807	Sequence 39807, A
11	6	2.6	93	10	US-09-864-761-36370	Sequence 36370, A
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17	6	2.6	151	10	US-09-883-985-10	Sequence 10, Appl
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19	6	2.6	172	9	US-09-738-626-5653	Sequence 5653, Ap
20	6	2.6	189	10	US-09-764-864-1255	Sequence 1255, Ap
21	6	2.6	194	9	US-09-791-932-104	Sequence 104, App
22	6	2.6	204	10	US-09-815-242-10054	Sequence 10054, A
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25	6	2.6	223	12	US-10-052-586-210	Sequence 210, App
26	6	2.6	255	10	US-09-815-242-13787	Sequence 13787, A
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29	6	2.6	265	10	US-09-888-623-2	Sequence 2, Appli
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58	6	2.6	347	9	US-09-902-853-148	Sequence 148, App
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62	6	2.6	347	10	US-09-909-320-148	Sequence 148, App
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ALIGNMENTS

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; Sequence 2, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Kindsvogel, Wayne
;  APPLICANT:  Chen, Zhi
;  TITLE OF INVENTION:  Human Cytokine Receptor
;  FILE REFERENCE:  99-93
;  CURRENT APPLICATION NUMBER: US/09/728,911
;  CURRENT FILING DATE:  2000-12-01
;  PRIOR APPLICATION NUMBER:  US 60/169,049
;  PRIOR FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER:  US 60/232,219
;  PRIOR FILING DATE:  2000-09-13
;  PRIOR APPLICATION NUMBER:  US 60/244,610
;  PRIOR FILING DATE:  2000-10-31
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 231
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-728-911-2

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; Sequence 6, Application US/09949192
; Patent No. US20020142292A1
; GENERAL INFORMATION:
;  APPLICANT: Parham, Christi L.
;  APPLICANT:  Gorman, Daniel L.
;  APPLICANT:  Kurata, Hirokazu
;  APPLICANT:  Arai, Naoko
;  APPLICANT:  Sana, Theodore R.
;  APPLICANT:  Mattson, Jeanine D.
;  APPLICANT:  Murphy, Erin E.
;  APPLICANT:  Savkoor, Chetan
;  APPLICANT:  Grein, Jeffery
;  APPLICANT:  Smith, Kathleen M.
;  APPLICANT:  McClanahan, Terrill K.
;  TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX01169K
;  CURRENT APPLICATION NUMBER: US/09/949,192
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,267
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 53
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RESULT 3
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; Sequence 13, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Kindsvogel, Wayne
;  APPLICANT:  Chen, Zhi
;  TITLE OF INVENTION:  Human Cytokine Receptor
;  FILE REFERENCE:  99-93
;  CURRENT APPLICATION NUMBER: US/09/728,911
;  CURRENT FILING DATE:  2000-12-01
;  PRIOR APPLICATION NUMBER:  US 60/169,049
;  PRIOR FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER:  US 60/232,219
;  PRIOR FILING DATE:  2000-09-13
;  PRIOR APPLICATION NUMBER:  US 60/244,610
;  PRIOR FILING DATE:  2000-10-31
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 13
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-728-911-13

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GenCore version 5.1.3

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Perfect score: 231
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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	6	2.6	43	4	US-08-470-106-35	Sequence 35, Appl
7	6	2.6	45	3	US-08-318-794-26	Sequence 26, Appl
8	6	2.6	45	4	US-08-470-106-26	Sequence 26, Appl
9	6	2.6	63	4	US-09-300-008B-42	Sequence 42, Appl
10	6	2.6	76	2	US-08-726-306A-30	Sequence 30, Appl
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26	6	2.6	148	3	US-08-513-974B-336	Sequence 336, App
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38	6	2.6	211	3	US-08-853-194-19	Sequence 19, Appl
39	6	2.6	221	4	US-09-382-155-17	Sequence 17, Appl
40	6	2.6	221	4	US-09-074-044A-17	Sequence 17, Appl
41	6	2.6	223	2	US-08-869-793-6	Sequence 6, Appli
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43	6	2.6	260	6	5223425-10	Patent No. 5223425
44	6	2.6	263	4	US-09-134-001C-5112	Sequence 5112, Ap
45	6	2.6	268	4	US-09-032-215-42	Sequence 42, Appl
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48	6	2.6	304	2	US-08-487-031-5	Sequence 5, Appli
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51	6	2.6	317	1	US-07-709-949-2	Sequence 2, Appli
52	6	2.6	317	4	US-08-729-594A-37	Sequence 37, Appl
53	6	2.6	317	4	US-08-937-993-37	Sequence 37, Appl
54	6	2.6	322	1	US-08-118-270-75	Sequence 75, Appl
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58	6	2.6	330	3	US-08-473-034-10	Sequence 10, Appl
59	6	2.6	330	4	US-09-197-344-1	Sequence 1, Appli
60	6	2.6	331	1	US-08-134-570-12	Sequence 12, Appl
61	6	2.6	342	2	US-08-845-295A-3	Sequence 3, Appli
62	6	2.6	342	3	US-09-140-933-3	Sequence 3, Appli
63	6	2.6	342	4	US-09-146-661-3	Sequence 3, Appli
64	6	2.6	342	4	US-09-150-515-3	Sequence 3, Appli
65	6	2.6	342	4	US-09-134-001C-5428	Sequence 5428, Ap
66	6	2.6	346	3	US-09-034-916-2	Sequence 2, Appli
67	6	2.6	347	4	US-09-188-930-326	Sequence 326, App
68	6	2.6	352	4	US-09-443-184-56	Sequence 56, Appl
69	6	2.6	361	4	US-09-556-877-299	Sequence 299, App
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72	6	2.6	369	1	US-07-816-283-8	Sequence 8, Appli
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75	6	2.6	369	1	US-08-417-103-16	Sequence 16, Appl
76	6	2.6	369	2	US-08-411-859-3	Sequence 3, Appli
77	6	2.6	369	4	US-08-120-601B-9	Sequence 9, Appli
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94	6	2.6	391	4	US-08-120-601B-8	Sequence 8, Appli
95	6	2.6	394	4	US-09-656-952-20	Sequence 20, Appl
96	6	2.6	398	3	US-09-189-035-6	Sequence 6, Appli
97	6	2.6	398	4	US-09-382-086-6	Sequence 6, Appli
98	6	2.6	405	2	US-08-881-857-2	Sequence 2, Appli
99	6	2.6	405	4	US-09-233-342A-2	Sequence 2, Appli
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ALIGNMENTS

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;Patent No. 5177189
;     APPLICANT: DYER, CHERYL A.;CURTISS, LINDA K.;SMITH, RICHARD
;     TITLE OF INVENTION: POLYPEPTIDE ANALOGS OF APOLIPOPROTEIN E
;     NUMBER OF SEQUENCES: 11
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/395,732
;       FILING DATE: 18-AUG-1989
;SEQ ID NO:11:
;       LENGTH: 30
5177189-11

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Qy     101 GRVRAA 106
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Db      15 GRVRAA 20


RESULT 2
5182364-12
;Patent No. 5182364
;     APPLICANT: DYER, CHERYL A.;CURTISS, LINDA K.;SMITH, RICHARD
;     TITLE OF INVENTION: POLYPEPTIDE ANALOGS OF APOLIPOPROTEIN E
;     NUMBER OF SEQUENCES: 14
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/485,158
;       FILING DATE: 26-FEB-1990
;SEQ ID NO:12:
;       LENGTH: 30
5182364-12

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  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 GRVRAA 106
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Db      15 GRVRAA 20


RESULT 3
US-08-023-980B-36
; Sequence 36, Application US/08023980B
; Patent No. 5843641
;  GENERAL INFORMATION:
;     APPLICANT:  Brown, Robert
;     APPLICANT:  Horvitz, H. Robert
;     APPLICANT:  Rosen, Daniel R.
;     TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
;     TITLE OF INVENTION:  TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
;     NUMBER OF SEQUENCES:  45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Clark & Elbing LLP
;       STREET:  585 Commercial Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109-1024
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/023,980B
;       FILING DATE:  26-FEB-1993
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clark, Paul T.
;       REGISTRATION NUMBER:  30,162
;       REFERENCE/DOCKET NUMBER:  00786/177001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617/723-4123
;       TELEFAX:  617/723-8962
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  39 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-023-980B-36

  Query Match             2.6%;  Score 6;  DB 2;  Length 39;
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Qy     160 NVSIED 165
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Db      17 NVSIED 22


RESULT 4
US-08-486-953A-31
; Sequence 31, Application US/08486953A
; Patent No. 5849290
;  GENERAL INFORMATION:
;     APPLICANT:  Brown, Robert
;     APPLICANT:  Horvitz, H. Robert
;     APPLICANT:  Rosen, Daniel R.
;     TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
;     TITLE OF INVENTION:  TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
;     NUMBER OF SEQUENCES:  53
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Clark & Elbing LLP
;       STREET:  176 Federal Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  FastSeq
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/486,953A
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/204,052
;       FILING DATE:  28-FEB-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clark, Paul T.
;       REGISTRATION NUMBER:  30,162
;       REFERENCE/DOCKET NUMBER:  00786/223002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617/428-0200
;       TELEFAX:  617/428-7045
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  39 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
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GenCore version 5.1.3

OM protein - protein search, using sw model

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Perfect score: 231
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
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9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
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14: sp_unclassified:*
15: sp_rvirus:*
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17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	165	71.4	263	4	Q969J5	Q969j5 homo sapien
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5	8	3.5	698	11	Q8R322	Q8r322 mus musculu
6	8	3.5	699	11	Q9D4A6	Q9d4a6 mus musculu
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ALIGNMENTS

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AC Q96A41;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Soluble cytokine class II receptor, short isoform precursor
DE (Interleukin 22-binding protein CRF2-10) (Class II cytokine receptor)
DE (Interleukin-22 binding protein).
GN CRF2-S1 OR IL22BP OR IL22RA2 OR IL-22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RX MEDLINE=21518574; PubMed=11607789;
RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
RA Wolk K., Asadullah K., Sabat R.;
RT "A novel, soluble homologue of the human IL-10 receptor with
RT preferential expression in placenta.";
RL Genes Immun. 2:329-334(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
RT receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396522; PubMed=11481447;
RA Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,
RA Yao L., Whitmore T.E., Chandrasekher Y., Grant F.J., Maurer M.,
RA Jelinek L., Storey H., Brender T., Hammond A., Topouzis S.,
RA Clegg C.H., Foster D.C.;
RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally
RT occurring IL-22 antagonist.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST;
RA Dumoutier L., Lejeune D., Renauld J.C.;
RT "Cloning and characterization of Interelukin-22 Binding Protein (IL-
RT 22BP), a natural antagonist of IL-TIF/IL-22.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ313161; CAC85634.1; -.
DR EMBL; AY040566; AAK85714.1; -.
DR EMBL; AY044429; AAK91775.1; -.
DR EMBL; AJ297262; CAC83097.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 231 SOLUBLE CYTOKINE CLASS II RECEPTOR, SHORT
FT ISOFORM.
SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;

Query Match 100.0%; Score 231; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.1e-234;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
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Db     61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL 180

Qy    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
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RESULT 2
Q969J5
ID Q969J5 PRELIMINARY; PRT; 263 AA.
AC Q969J5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Soluble cytokine class II receptor, long isoform precursor
DE (Interleukin 22-binding protein CRF2-10L).
GN CRF2-S1 OR IL22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=21518574; PubMed=11607789;
RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
RA Wolk K., Asadullah K., Sabat R.;
RT "A novel, soluble homologue of the human IL-10 receptor with
RT preferential expression in placenta.";
RL Genes Immun. 2:329-334(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
RT receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103(2001).
DR EMBL; AJ313162; CAC85635.1; -.
DR EMBL; AY040567; AAK85715.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 263 SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG
FT ISOFORM.
SQ SEQUENCE 263 AA; 30550 MW; C96ECEC5D78AC79B CRC64;

Query Match 71.4%; Score 165; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 7.5e-165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     67 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     99 YGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWET 158
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Qy     127 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 KIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKV 218

Qy     187 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 231
           |||||||||||||||||||||||||||||||||||||||||||||
Db     219 YEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP 263


RESULT 3
Q96QR0
ID   Q96QR0      PRELIMINARY;      PRT;   130 AA.
AC   Q96QR0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin 22-binding protein CRF2-10S.
GN   IL22BP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21286453; PubMed=11390454;
RA   Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA   Dickensheets H., Donnelly R.P., Pestka S.;
RT   "Identification, cloning, and characterization of a novel soluble
RT   receptor that binds IL-22 and neutralizes its activity.";
RL   J. Immunol. 166:7096-7103(2001).
DR   EMBL; AY040568; AAK85716.1; -.
DR   InterPro; IPR000282; Cytok_receptor_2.
SQ   SEQUENCE   130 AA;  15128 MW;  A165814C641F5E5B CRC64;

  Query Match             54.1%;  Score 125;  DB 4;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-123;
  Matches  125;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY 60

Qy      61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120
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Db      61 FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF 120

Qy     121 TPWWE 125
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Db     121 TPWWE 125


RESULT 4
Q9HKC4
ID   Q9HKC4      PRELIMINARY;      PRT;   121 AA.
AC   Q9HKC4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Hypothetical membrane protein.
GN   TA0677.
OS   Thermoplasma acidophilum.
OC   Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC   Thermoplasmataceae; Thermoplasma.
OX   NCBI_TaxID=2303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DSM 1728;
RX   MEDLINE=20479972; PubMed=11029001;
RA   Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA   Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT   "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT   acidophilum.";
RL   Nature 407:508-513(2000).
DR   EMBL; AL445065; CAC11815.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   121 AA;  13083 MW;  3C80DC4C2B04FD39 CRC64;

  Query Match             3.5%;  Score 8;  DB 17;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     139 NGSLLVIL 146
           ||||||||
Db      77 NGSLLVIL 84


RESULT 5
Q8R322
ID   Q8R322      PRELIMINARY;      PRT;   698 AA.
AC   Q8R322;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 4933405K21 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026797; AAH26797.1; -.
SQ   SEQUENCE   698 AA;  79560 MW;  22E5E7217AA4D333 CRC64;

  Query Match             3.5%;  Score 8;  DB 11;  Length 698;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 GTQSTHES 28
           ||||||||
Db     106 GTQSTHES 113


RESULT 6
Q9D4A6
ID   Q9D4A6      PRELIMINARY;      PRT;   699 AA.
AC   Q9D4A6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   4933405K21Rik protein.
GN   4933405K21RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TESTIS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK016671; BAB30371.1; -.
DR   MGD; MGI:1921662; 4933405K21Rik.
SQ   SEQUENCE   699 AA;  79574 MW;  5403C38F9DC7ED75 CRC64;

  Query Match             3.5%;  Score 8;  DB 11;  Length 699;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 GTQSTHES 28
           ||||||||
Db     107 GTQSTHES 114


RESULT 7
Q8ZKM7
ID   Q8ZKM7      PRELIMINARY;      PRT;   833 AA.
AC   Q8ZKM7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   General PTS family, enzyme I (EC 2.7.3.9).
GN   PTSA OR STM4110.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
DR   EMBL; AE008892; AAL22950.1; -.
DR   InterPro; IPR001020; HPr_HisP_site.
DR   InterPro; IPR000032; HPr_protein.
DR   InterPro; IPR000121; PEP_utilizers.
DR   InterPro; IPR004715; PTSIIA_fruc.
DR   InterPro; IPR002178; PTS_EIIA_2.
DR   Pfam; PF00391; PEP-utilizers; 1.
DR   Pfam; PF02896; PEP-utilizers_C; 1.
DR   Pfam; PF00381; PTS-HPr; 1.
DR   Pfam; PF00359; PTS_EIIA_2; 1.
DR   ProDom; PD000940; PEP_utilizers; 1.
DR   ProDom; PD001689; PTS_EIIA_2; 1.
DR   TIGRFAMs; TIGR00848; fruA; 1.
DR   PROSITE; PS00742; PEP_ENZYMES_2; 1.
DR   PROSITE; PS00370; PEP_ENZYMES_PHOS_SITE; 1.
DR   PROSITE; PS00369; PTS_HPR_HIS; 1.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   833 AA;  92082 MW;  D2FE53D3DD81D6BF CRC64;

  Query Match             3.5%;  Score 8;  DB 16;  Length 833;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     194 VEIEALTP 201
           ||||||||
Db     317 VEIEALTP 324


RESULT 8
Q8TUL7
ID   Q8TUL7      PRELIMINARY;      PRT;   83 AA.
AC   Q8TUL7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein MA0049.
GN   MA0049.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE010661; AAM03503.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   83 AA;  9796 MW;  EF0CF4C7F28B098F CRC64;

  Query Match             3.0%;  Score 7;  DB 17;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     140 GSLLVIL 146
           |||||||
Db      65 GSLLVIL 71


RESULT 9
Q8TNM9
ID   Q8TNM9      PRELIMINARY;      PRT;   127 AA.
AC   Q8TNM9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Response regulator receiver.
GN   MA4671.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:43:26 ; Search time 11 Seconds
(without alignments)
871.003 Million cell updates/sec

Title: US-09-728-911-2
Perfect score: 231
Sequence: 1 MMPKHCFLGFLISFFLTGVA.....YQPMLDRRSQRSEERCVEIP 231

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	7	3.0	208	1	HIS1_LACLA	Q02129	lactococcus
2	7	3.0	213	1	HIS5_LEGPN	Q9rdx3	legionella
3	7	3.0	270	1	CXB3_HUMAN	O75712	homo sapien
4	7	3.0	297	1	RLA0_METVO	Q9y8j3	methanococc
5	7	3.0	303	1	TTDA_ECOLI	P05847	escherichia
6	7	3.0	341	1	RIR2_HELPY	P55983	helicobacte
7	7	3.0	457	1	YIR0_YEAST	P40441	saccharomyc
8	7	3.0	535	1	ORC2_SCHPO	Q09142	schizosacch
9	7	3.0	546	1	GHT5_SCHPO	P78831	schizosacch
10	7	3.0	567	1	HXT9_YEAST	P40885	saccharomyc
11	7	3.0	567	1	HXTA_YEAST	P54862	saccharomyc
12	7	3.0	570	1	HXT1_YEAST	P32465	saccharomyc
13	7	3.0	592	1	HXT5_YEAST	P38695	saccharomyc
14	7	3.0	637	1	FTSH_RICCN	Q92jj9	rickettsia
15	7	3.0	637	1	FTSH_RICPR	Q9zea2	rickettsia
16	7	3.0	812	1	LON_BRUAB	O52605	brucella ab
17	7	3.0	1166	1	RPA2_EUPOC	P28365	euplotes oc
18	7	3.0	4273	1	PKSM_BACSU	P40872	bacillus su
19	6	2.6	65	1	BB12_SCHCO	P78743	schizophyll
20	6	2.6	91	1	Y022_ARCFU	O30213	archaeoglob
21	6	2.6	119	1	EYA1_CHICK	Q9yha0	gallus gall
22	6	2.6	119	1	EYA4_CHICK	Q9yh98	gallus gall
23	6	2.6	125	1	YSH6_CAEEL	Q09947	caenorhabdi
24	6	2.6	128	1	YF75_MYCPN	P75204	mycoplasma
25	6	2.6	134	1	CYB_ANOCU	Q31684	anoura caud
26	6	2.6	134	1	CYB_STUTI	Q35942	sturnira ti
27	6	2.6	139	1	CDRB_CLOAB	Q45811	clostridium
28	6	2.6	144	1	NU6M_ASCSU	P24873	ascaris suu
29	6	2.6	145	1	PSAN_HORVU	P31093	hordeum vul
30	6	2.6	152	1	SODC_CAVPO	P33431	cavia porce
31	6	2.6	153	1	SODC_MOUSE	P08228	mus musculu
32	6	2.6	153	1	SODC_RAT	P07632	rattus norv
33	6	2.6	157	1	NUSB_XYLFA	Q9pes3	xylella fas
34	6	2.6	161	1	PHAB_SYNEL	P50031	synechococc
35	6	2.6	161	1	PHAB_SYNY3	Q01952	synechocyst
36	6	2.6	161	1	PHAB_SYNY4	Q02924	synechocyst
37	6	2.6	162	1	PHAB_FREDI	P16571	fremyella d
38	6	2.6	166	1	MEG3_ARATH	Q9fh13	arabidopsis
39	6	2.6	176	1	CYB_NYCHU	Q36572	nycticeius
40	6	2.6	176	1	CYB_STULI	Q35873	sturnira li
41	6	2.6	182	1	PGRP_TRINI	O76537	trichoplusi
42	6	2.6	185	1	BCNA_CLOPE	P15935	clostridium
43	6	2.6	195	1	OAZ3_MOUSE	Q9r109	mus musculu
44	6	2.6	203	1	RECR_MYCLE	O69520	mycobacteri
45	6	2.6	204	1	YAGU_ECOLI	P77262	escherichia
46	6	2.6	207	1	GSPJ_AERHY	P31739	aeromonas h
47	6	2.6	214	1	KAD_MYCPU	Q98q02	mycoplasma
48	6	2.6	215	1	Y473_AQUAE	O66771	aquifex aeo
49	6	2.6	216	1	HIS2_THEET	Q9rpq3	thermoanaer
50	6	2.6	219	1	GSHE_PIG	O18994	sus scrofa
51	6	2.6	220	1	RECR_DEIRA	Q9zna2	deinococcus
52	6	2.6	221	1	GSHE_CANFA	O46607	canis famil
53	6	2.6	221	1	GSHE_HUMAN	O75715	homo sapien
54	6	2.6	221	1	GSHE_MACFA	P28714	macaca fasc
55	6	2.6	230	1	RNS1_ARATH	P42813	arabidopsis
56	6	2.6	232	1	SOML_PROAN	O73847	protopterus
57	6	2.6	234	1	DNAJ_RHILE	O33529	rhizobium l
58	6	2.6	234	1	PUR7_PYRAE	Q8zzk5	pyrobaculum
59	6	2.6	234	1	YRJE_LACLA	Q9ceu8	lactococcus
60	6	2.6	239	1	FRDB_WOLSU	P17596	wolinella s
61	6	2.6	243	1	ZIPA_XYLFA	Q9pag1	xylella fas
62	6	2.6	244	1	PHOS_MOUSE	Q9qw08	mus musculu
63	6	2.6	246	1	PHOS_RAT	P20942	rattus norv
64	6	2.6	254	1	YFA6_YEAST	P43584	saccharomyc
65	6	2.6	255	1	TPIS_SALTI	Q8z2y2	salmonella
66	6	2.6	255	1	TPIS_SALTY	Q8zkp7	salmonella
67	6	2.6	259	1	CFAD_MOUSE	P03953	mus musculu
68	6	2.6	259	1	DEF3_DERFA	P49275	dermatophag
69	6	2.6	259	1	Y305_CHLMU	Q9pl03	chlamydia m
70	6	2.6	271	1	PSB8_RAT	P28064	rattus norv
71	6	2.6	272	1	ESL3_MYCPN	P75268	mycoplasma
72	6	2.6	276	1	PSB8_HUMAN	P28062	homo sapien
73	6	2.6	278	1	P29K_STRPN	P42362	streptococc
74	6	2.6	280	1	P29K_STRPA	P31309	streptococc
75	6	2.6	285	1	CABA_MOUSE	Q99020	mus musculu
76	6	2.6	285	1	YOY9_CAEEL	P34666	caenorhabdi
77	6	2.6	289	1	CWFN_SCHPO	Q9p7c6	schizosacch
78	6	2.6	289	1	TF_CAVPO	Q9jlu8	cavia porce
79	6	2.6	290	1	NIH2_AZOCH	P06118	azotobacter
80	6	2.6	292	1	FIXA_RHIME	P09818	rhizobium m
81	6	2.6	294	1	NIFH_BRAJA	P06117	bradyrhizob
82	6	2.6	294	1	NIFH_BRASP	P00463	bradyrhizob
83	6	2.6	297	1	YG1B_YEAST	P53210	saccharomyc
84	6	2.6	299	1	PUR7_STRCO	Q9rkl1	streptomyce
85	6	2.6	302	1	RPO4_FOWPV	Q9j540	fowlpox vir
86	6	2.6	303	1	PQQB_PSEFL	P55172	pseudomonas
87	6	2.6	305	1	CDSA_MYCGE	Q49433	m putative
88	6	2.6	305	1	TNE2_HUMAN	O95859	homo sapien
89	6	2.6	309	1	KHSE_BUCAI	O66132	buchnera ap
90	6	2.6	317	1	APE_HUMAN	P02649	homo sapien
91	6	2.6	317	1	APE_MACFA	P10517	macaca fasc
92	6	2.6	317	1	APE_PAPAN	P05770	papio anubi
93	6	2.6	322	1	GRP2_MOUSE	O89100	m grb2-rela
94	6	2.6	326	1	UNG2_HUMAN	P22674	homo sapien
95	6	2.6	329	1	YA90_MYCPN	P75603	mycoplasma
96	6	2.6	330	1	GRP2_HUMAN	O75791	h grb2-rela
97	6	2.6	330	1	ODBA_BACSU	P37940	bacillus su
98	6	2.6	331	1	GALR_LACCA	O84905	lactobacill
99	6	2.6	341	1	RIR2_HELPJ	Q9zkc3	helicobacte
100	6	2.6	342	1	ARGC_STRCO	P54895	streptomyce

ALIGNMENTS

RESULT 1

```
HIS1_LACLA
ID   HIS1_LACLA     STANDARD;      PRT;   208 AA.
AC   Q02129; Q9CG94;
DT   01-JUL-1993 (Rel. 26, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   ATP phosphoribosyltransferase (EC 2.4.2.17).
GN   HISG OR LL1208.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCDO 2118;
RX   MEDLINE=93015709; PubMed=1400209;
RA   Delorme C., Ehrlich S.D., Renault P.;
RT   "Histidine biosynthesis genes in Lactococcus lactis subsp. lactis.";
RL   J. Bacteriol. 174:6571-6579(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=99362697; PubMed=10430882;
RA   Sissler M., Delorme C., Bond J., Ehrlich S.D., Renault P.,
RA   Francklyn C.;
RT   "An aminoacyl-tRNA synthetase paralog with a catalytic role in
RT   histidine biosynthesis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:8985-8990(1999).
CC   -!- CATALYTIC ACTIVITY: 1-(5-phospho-D-ribosyl)-ATP + diphosphate =
CC       ATP + 5-phospho-alpha-D-ribose 1-diphosphate.
CC   -!- PATHWAY: Histidine biosynthesis; first step. Very important in the
CC       regulation of histidine metabolism.
CC   -!- SUBUNIT: Homohexamer (By similarity). Binds to hisZ possibly to
CC       allow the regulation of hisG transferase activity by histidine.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- DOMAIN: Lacks the C-terminal regulatory region which is replaced
CC       by hisZ.
CC   -!- SIMILARITY: BELONGS TO THE ATP PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC       SHORT SUBFAMILY.
CC   -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC       frameshift in position 174.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U92974; AAB81903.1; -.
DR   EMBL; AE006353; AAK05306.1; ALT_FRAME.
DR   PIR; S28532; S28532.
DR   PIR; D45734; D45734.
DR   InterPro; IPR001348; HisG.
DR   Pfam; PF01634; HisG; 1.
DR   ProDom; PD003516; HisG; 1.
DR   TIGRFAMs; TIGR00070; hisG; 1.
DR   PROSITE; PS01316; ATP_P_PHORIBOSYLTR; 1.
KW   Histidine biosynthesis; Transferase; Glycosyltransferase;
KW   Complete proteome.
FT   CONFLICT     51     51       P -> A (IN REF. 1).
FT   CONFLICT     86     86       Y -> D (IN REF. 1).
FT   CONFLICT    110    110       H -> R (IN REF. 1).
SQ   SEQUENCE   208 AA;  23677 MW;  8CE4CD0A16D39FEF CRC64;
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  Query Match             3.0%;  Score 7;  DB 1;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     165 DYYELLY 171
           |||||||
Db      80 DYYELLY 86
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```
RESULT 2
HIS5_LEGPN
ID   HIS5_LEGPN     STANDARD;      PRT;   213 AA.
AC   Q9RDX3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP
DE   synthase glutamine amidotransferase subunit) (IGP synthase subunit
DE   hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH).
GN   HISH.
OS   Legionella pneumophila.
OC   Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=446;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RC1 / Olda / Serogroup 1;
RA   Lueneberg E., Zetzmann N., Hartmann M., Knirel Y.A., Kooistra O.,
RA   Zaehringer U., Helbig J., Frosch M.;
RT   "A 30 kb gene cluster involved in biosynthesis of the virulence
RT   associated lipopolysaccharide carbohydrate moiety of Legionella
RT   pneumophila.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
CC       IGP, AICAR and glutamate. The hisH subunit provides the glutamine
CC       amidotransferase activity that produces the ammonia necessary to
CC       hisF for the synthesis of IGP and AICAR (By similarity).
CC   -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-
CC       ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
CC       carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-
CC       aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC   -!- PATHWAY: Histidine biosynthesis; fifth step.
CC   -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ007311; CAB65214.1; -.
DR   InterPro; IPR000991; GATase_1.
DR   Pfam; PF00117; GATase; 1.
DR   PROSITE; PS00442; GATASE_TYPE_I; 1.
KW   Histidine biosynthesis; Transferase; Glutamine amidotransferase.
FT   ACT_SITE     81     81       BY SIMILARITY.
FT   ACT_SITE    195    195       BY SIMILARITY.
FT   ACT_SITE    197    197       BY SIMILARITY.
SQ   SEQUENCE   213 AA;  23310 MW;  F27CDEFD7C771D7C CRC64;
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  Query Match             3.0%;  Score 7;  DB 1;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      56 NSSVYFV 62
           |||||||
Db     150 NSSVYFV 156
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:44:46 ; Search time 20 Seconds
(without alignments)
1110.353 Million cell updates/sec

Title: US-09-728-911-2
Perfect score: 231
Sequence: 1 MMPKHCFLGFLISFFLTGVA.....YQPMLDRRSQRSEERCVEIP 231

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

W[redacted]size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	3.0	180	2	H86775	ATP phosphoribosyl
2	7	3.0	213	2	B86845	hypothetical prote
3	7	3.0	218	2	T49885	peptide methionine
4	7	3.0	236	2	A98351	agropine synthesis
5	7	3.0	236	2	AE2931	agropine synthesis
6	7	3.0	241	2	B95856	hypothetical prote
7	7	3.0	243	2	AC2727	hypothetical prote
8	7	3.0	243	2	G97508	hypothetical prote
9	7	3.0	255	2	H72319	mazG protein - The
10	7	3.0	270	2	JE0274	connexin 31 - huma
11	7	3.0	303	1	QQECRT	L(+)-tartrate dehy
12	7	3.0	303	2	H91121	L-tartrate dehydra
13	7	3.0	303	2	G85966	L-tartrate dehydra
14	7	3.0	304	2	T32718	hypothetical prote
15	7	3.0	312	2	T35400	probable phytoene
16	7	3.0	322	2	AC3207	conserved hypothet
17	7	3.0	333	2	B90172	conserved hypothet
18	7	3.0	341	2	D64565	ribonucleoside dip
19	7	3.0	357	2	H70346	undecaprenyl-phosp
20	7	3.0	371	2	T42623	probable sugar tra
21	7	3.0	393	2	AE3164	conserved hypothet
22	7	3.0	446	2	H90094	hypothetical prote
23	7	3.0	448	2	E96991	Na+/H+ antiporter,
24	7	3.0	457	2	S50357	sugar transport pr
25	7	3.0	479	2	T48025	hypothetical prote
26	7	3.0	512	2	B69146	gluthatione-regula
27	7	3.0	535	2	S68446	origin recognition
28	7	3.0	546	2	T40888	probable glucose t
29	7	3.0	552	2	G96729	hypothetical prote
30	7	3.0	562	2	E72608	probable hyuB APE1
31	7	3.0	567	2	S50708	hexose transport p
32	7	3.0	567	2	S49600	glucose transport
33	7	3.0	570	2	S38798	hexose transport p
34	7	3.0	592	2	S43742	hexose transport p
35	7	3.0	637	2	C71712	cell division prot
36	7	3.0	637	2	D97708	cell division prot
37	7	3.0	788	2	T26967	hypothetical prote
38	7	3.0	800	2	I51653	dsRNA-binding prot
39	7	3.0	823	2	AF3361	endopeptidase La (
40	7	3.0	921	2	G71705	alkaline phosphata
41	7	3.0	1166	2	S70413	DNA-directed RNA p
42	7	3.0	1210	2	A48001	phospholipase C (E
43	7	3.0	2825	2	T14271	Doc4 protein, stre
44	7	3.0	4273	2	C69679	polyketide synthas
45	6	2.6	33	2	A60465	cytochrome P450 D1
46	6	2.6	56	2	F95077	hypothetical prote
47	6	2.6	56	2	B97945	hypothetical prote
48	6	2.6	57	2	AH2906	conserved hypothet
49	6	2.6	82	2	E70972	probable enoyl-coA
50	6	2.6	90	2	H95138	hypothetical prote
51	6	2.6	90	2	H98006	hypothetical prote
52	6	2.6	91	2	F69252	hypothetical prote
53	6	2.6	93	2	H81357	hypothetical prote
54	6	2.6	94	2	AB0949	hypothetical prote
55	6	2.6	102	2	H87678	hypothetical prote
56	6	2.6	116	2	G84374	hypothetical prote
57	6	2.6	118	2	C90583	50S ribosomal prot
58	6	2.6	121	2	S71007	hypothetical prote
59	6	2.6	125	2	T16042	hypothetical prote
60	6	2.6	127	2	PN0464	hypothetical prote
61	6	2.6	128	2	S73593	hypothetical prote
62	6	2.6	134	2	B95216	conserved hypothet
63	6	2.6	136	2	S74683	hypothetical prote
64	6	2.6	139	2	I40604	hypothetical prote
65	6	2.6	141	2	S10037	hypothetical prote
66	6	2.6	141	2	H98079	conserved hypothet
67	6	2.6	143	2	H81077	hypothetical prote
68	6	2.6	144	2	S26014	NADH2 dehydrogenas
69	6	2.6	145	2	S35159	photosystem I chai
70	6	2.6	148	2	T04727	hypothetical prote
71	6	2.6	152	2	S36108	superoxide dismuta
72	6	2.6	152	2	G87539	phosphotyrosine pr
73	6	2.6	154	2	JQ0915	superoxide dismuta
74	6	2.6	154	2	JC1192	superoxide dismuta
75	6	2.6	156	1	D69019	conserved hypothet
76	6	2.6	157	2	D82741	transcription term
77	6	2.6	159	2	T15627	hypothetical prote
78	6	2.6	159	2	AE1241	B. subtilis YqzC p
79	6	2.6	159	2	AI1603	B. subtilis YqzC p
80	6	2.6	160	2	A83110	hypothetical prote
81	6	2.6	161	2	B44462	allophycocyanin be
82	6	2.6	161	2	S33624	allophycocyanin be
83	6	2.6	161	2	E48232	cysteine-rich exte
84	6	2.6	162	2	C31385	allophycocyanin 1
85	6	2.6	164	2	A81325	probable signal-tr
86	6	2.6	165	2	C48232	cysteine-rich exte
87	6	2.6	165	2	G95074	PTS system IIA com
88	6	2.6	166	2	F86898	single-strand bind
89	6	2.6	169	2	F72465	hypothetical prote
90	6	2.6	172	2	F83071	probable transcrip
91	6	2.6	173	2	S41755	cyclin E type II -
92	6	2.6	173	2	B97942	hypothetical prote
93	6	2.6	175	2	D86180	hypothetical prote
94	6	2.6	177	2	T36271	probable RNA polym
95	6	2.6	178	2	S54444	prepilin 18.1K typ
96	6	2.6	178	2	E88637	protein W09G12.6 [
97	6	2.6	180	2	PC1305	genome polyprotein
98	6	2.6	180	2	F71809	hypothetical prote
99	6	2.6	180	2	B64711	purine nucleoside
100	6	2.6	183	2	E83410	probable transcrip

ALIGNMENTS

RESULT 1
H86775
ATP phosphoribosyltransferase (EC 2.4.2.17) [imported] - Lactococcus lactis subsp. lacti
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: H86775
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86775
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180 <STO>
A;Cross-references: GB:AE005176; PID:g12724177; PIDN:AAK05306.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: hisG
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 3.0%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 DYYELLY 171
|||||||
Db 80 DYYELLY 86

RESULT 2
B86845
hypothetical protein yscB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: B86845
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86845
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: GB:AE005176; PID:g12724784; PIDN:AAK05860.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yscB

Query Match 3.0%; Score 7; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FLGFLIS 13
|||||||
Db 44 FLGFLIS 50

RESULT 3
T49885
peptide methionine sulfoxide reductase-like protein - Arabidopsis thaliana
N;Alternate names: protein T2I1.170
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C;Accession: T49885
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24493
A;Accession: T49885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <BEV>
A;Cross-references: EMBL:AL163912; GSPDB:GN00063; ATSP:T2I1.170
A;Experimental source: cultivar Columbia; BAC clone T2I1
C;Genetics:
A;Gene: ATSP:T2I1.170
A;Map position: 5
A;Introns: 135/3
C;Superfamily: peptide methionine sulfoxide reductase

Query Match 3.0%; Score 7; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 SLEKEQK 185
|||||||
Db 161 SLEKEQK 167

RESULT 4
A98351
agropine synthesis reductase [imported] - Agrobacterium tumefaciens (strain C5[redacted]reon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: A98351
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: A98351
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-236 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK90331.1; PID:g15160366; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_3508
A;Map position: linear chromosome
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.0%; Score 7; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 ASAGSYS 112
|||||||
Db 147 ASAGSYS 153

RESULT 5
AE2931
agropine synthesis reductase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AE2931
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE2931
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-236 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL43867.1; PID:g17741412; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: mas1
A;Map position: linear chromosome
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology